



SEQUENCE LISTING

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Hastings, Gregg
Rosen, Craig

<120> Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3
and 4

<130> PF140P1D1

<140> 09/613,508

<141> 2000-07-10

<150> US 08/462,969

<151> 1995-06-05

<150> US 08/334,251

<151> 1994-11-01

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 1

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gcgggggacac gggtcgcttt gggctcttcc acccctgcgg agcgcactac cccgagccag 180
gggcggtgca agccccgccc ggccctaccc agggcggtc ctccctccgc agcgccgaga 240
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cggtcctcgt ttgtaccgtc cctcttcagt aagaagaaga aaaatgtcac catgcgatcc 480
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ggcaaattgca tcataataaa caacaagaac tttgataaag tgacaggtat gggcgttcga 600
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 ggggtacatt ctagctgaga agcaatgggt cactcattaa tgaatcacat ttttttatgc 1320
 tcttgaaata ttcagaaatt ctccaggatt ttaatttcag gaaaatgtat t 1371

<210> 2
 <211> 303
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser
 1 5 10 15

Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val
 20 25 30

Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile
 35 40 45

Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe
 50 55 60

Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys
 65 70 75 80

Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala
 85 90 95

Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn
 100 105 110

Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu
 115 120 125

Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His
 130 135 140

Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys
 145 150 155 160

Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu
 165 170 175

Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
 180 185 190

Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn
 195 200 205

Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser

210

215

220

Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp
225 230 235 240

Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Glu Leu
245 250 255

Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His
260 265 270

Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile
275 280 285

Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln
290 295 300

<210> 3
<211> 1159
<212> DNA
<213> Homo sapiens

<400> 3
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gccgtgagga gttagcgagc cctgctcaca ctccggcgctc tggttttcgg tgggtgtgcc 180
ctgcacctgc ctcttccgc attctcatta ataaaggat ccatggagaa cactgaaaac 240
tcagtggatt caaaatccat taaaaatttg gaaccaaaga tcatacatgg aagcgaatca 300
atggactctg gaatatccct ggacaacagt tataaaatgg attatcctga gatgggttta 360
tgtataataa ttaataataa gaattttcat aaaagcactg gaatgacatc tcgggtctggt 420
acagatgtcg atgcagcaaa cctcagggaa acattcagaa acttgaaata tgaagtcagg 480
aataaaaatg atcttacacg tgaagaaatt gtggaattga tgcgtgatgt ttctaaagaa 540
gatcacagca aaaggagcag ttttgtttgt gtgcttctga gccatggtga agaaggaata 600
atttttggaa caaatggacc tgttgacctg aaaaaataa caaacttttt cagaggggat 660
cgtttagtaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca 720
gaactggact gtggcattga gacagacagt ggtgttgatg atgacatggc gtgtcataaa 780
ataccagtgg aggccgactt cttgtatgca tactccacag cacctggtta ttattcttgg 840
cgaaattcaa aggatggctc ctggttcatc cagtcgcttt gtgccatgct gaaacagtat 900
gccgacaagc ttgaatttat gcacattctt acccgggtta accgaaagggt ggcaacagaa 960
tttgagtcct tttcctttga cgctactttt catgcaaaga aacagattcc atgtattggt 1020
tccatgctca caaaagaact ctatttttat cactaaagaa atggttggtt ggtggttttt 1080
tttagtttgt atgccaagtg agaagatggt atatttgggt actgtatttc cctctcattg 1140
gggacctact ctcatgctg 1159

<210> 4
<211> 277
<212> PRT
<213> Homo sapiens

<400> 4

Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
1 5 10 15

Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
20 25 30

Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
35 40 45

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
50 55 60

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65 70 75 80

Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
85 90 95

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
100 105 110

Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115 120 125

Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe

255

<220>
 <223> Contains the ICE-LAP-3 translational initiation site ATG followed by 5 nucleotides of ICE-LAP-3 coding sequence starting from the initiation codon

<400> 9
 gactatgcgt gcggggacac gg 22

<210> 10
 <211> 53
 <212> DNA
 <213> Artificial

<220>
 <223> Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-3 coding sequence, not including the stop codon

<400> 10
 aatcaagcgt agtctgggac gtcgtatggg tattcaccct ggtggaggat ttg 53

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Contains the ICE-LAP-4 translational initiation site, ATG, followed by 15 nucleotides of ICE-LAP-4 coding sequence starting from the initiation codon

<400> 11
 accatggaga acactgaaaa c 21

<210> 12
 <211> 53
 <212> DNA
 <213> Artificial

<220>
 <223> Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-4 coding sequence, not including the stop codon

<400> 12
 aatcaagcgt agtctgggac gtcgtatggg tagtgataaa aatagagttc ttt 53

<210> 13
 <211> 503
 <212> PRT
 <213> Caenorhabditis elegans

<400> 13

Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met
 1 5 10 15

Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala
 20 25 30

Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly
 35 40 45

Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg
 50 55 60
 Gly Asp Val Ala Phe Asp Ala Phe Tyr Asp Ala Leu Arg Ser Thr Gly
 65 70 75 80
 His Glu Gly Leu Ala Glu Val Leu Glu Pro Leu Ala Arg Ser Val Asp
 85 90 95
 Ser Asn Ala Val Glu Phe Glu Cys Pro Met Ser Pro Ala Ser His Arg
 100 105 110
 Arg Ser Arg Ala Leu Ser Pro Ala Gly Tyr Thr Ser Pro Thr Arg Val
 115 120 125
 His Arg Asp Ser Val Ser Ser Val Ser Ser Phe Thr Ser Tyr Gln Asp
 130 135 140
 Ile Tyr Ser Arg Ala Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser
 145 150 155 160
 Ser Asp Arg His Asn Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser
 165 170 175
 Gln Pro Ser Ser Ala Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly
 180 185 190
 Tyr Ser Ser Ser Arg Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr
 195 200 205
 Gln Tyr Ile Phe His Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr
 210 215 220
 Ile Ser Arg Val Phe Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser
 225 230 235 240
 Pro Arg Gly Met Cys Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met
 245 250 255
 Pro Thr Arg Asn Gly Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu
 260 265 270
 Phe Arg Cys Met Gly Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly
 275 280 285
 Arg Gly Met Leu Leu Thr Ile Arg Asp Phe Ala Lys His Glu Ser His
 290 295 300
 Gly Asp Ser Ala Ile Leu Val Ile Leu Ser His Gly Glu Glu Asn Val
 305 310 315 320
 Ile Ile Gly Val Asp Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp

Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
 65 70 75 80
 Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly
 85 90 95
 Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro
 100 105 110
 Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly
 115 120 125
 Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile
 130 135 140
 Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser
 145 150 155 160
 Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile
 165 170 175
 Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu
 180 185 190
 Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala
 195 200 205
 Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His
 210 215 220
 Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg
 225 230 235 240
 Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu
 245 250 255
 Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser
 260 265 270
 Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Asp
 275 280 285
 Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn
 290 295 300
 Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys
 305 310 315 320
 Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp
 325 330 335

Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg
340 345 350

Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu
355 360 365

Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala
370 375 380

Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu
385 390 395 400

Phe Pro Gly His

312
Conclude